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    1981 gggcaagctt
//
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Feb 9 2005 14:31:10

EXHIBIT 5


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DEFINITION  alpha amylase [Geobacillus stearothermophilus].
ACCESSION   AAB86961
VERSION     AAB86961.1  GI:2642326
DBSOURCE    locus AF032864 accession AF032864.1
KEYWORDS    .
SOURCE      Geobacillus stearothermophilus
  ORGANISM  Geobacillus stearothermophilus
            Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
REFERENCE   1  (residues 1 to 549)
  AUTHORS   da Silva,A.C.R., Fernandes,E. and Pueyo,M.T.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-NOV-1997) Physiology, ICB, Av Prof Lineu Prestes, Sao
            Paulo, SP, Brasil
COMMENT     Method: conceptual translation supplied by author.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:1422"
     Protein         1..549
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     CDS             1..549
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                     /transl_table=11
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      121 aiqaahaagm qvyadvvfdh kggadgtewv davevnpsdr nqeisgtyqi qawtkfdfpg
      181 rgntyssfkw rwyhfdgvdw desrklsriy kfrgigkawd wevdtengny dylmyadldm
      241 dhpevvtelk nwgkwyvntt nidgfrldav khikfsffpd wlsyvrsqtg kplftvgeyw
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      541 teprlvawp
//
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EXHIBIT 6

ATCC 31,195 ALPHA-AMYLASE AMINO ACID SEQUENCE

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121 vnpsdrnqei sgtyqiqawt kfdfpgrgnt yssfkwrwyh fdgvdwdesr klsriykfrg
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241 fsffpdwlsy vrsqtgkplf tvgeywsydi nklhnyitkt ngtmslfdap lhnkfytask
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481 vprkttvst
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EXHIBIT G

IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE

NOVOZYMES A/S, Plaintiff v. GENENCOR INTERNATIONAL, INC., and ENZYME DEVELOPMENT CORPORATION Defendants	C.A. No. 05-160-KAJ

DECLARATION OF STEEN TROELS JØRGENSEN

I, Steen Troels Jørgensen, do hereby declare as follows:

1. I am a citizen of Denmark and am more than twenty-one (21) years of age.

2. I am a Senior Science Manager in the department of bacterial gene technology at Novozymes A/S ("Novozymes"), a position I have held since 2002. From 1995-2002, I held the position of Science Manager in the same department at either Novozymes or its predecessor, Novo Nordisk A/S. From 1985 to 1995 I was a scientist in that same department.

3. In 1985 I received the Danish equivalent of a U.S. Master's degree in biology from the University of Copenhagen in Denmark. My thesis for that degree was in the field of molecular biology.

4. Details of my education and professional experience are set forth in my *Curriculum Vitae*, which is submitted as Exhibit 1 along with this Declaration.

I. BACKGROUND

5. I understand that this Declaration is being submitted in support of a law suit between Novozymes A/S ("Novozymes"), and the parties Genencor International, Inc. ("Genencor") and Enzyme Development Corporation ("EDC"). In particular, I understand that Genencor and EDC have been accused of making and selling a product in the United States, called Spezyme Ethyl, that infringes a patent owned by Novozymes.

6. I have been given what I understand to be a sample of Genencor and EDC's Spezyme Ethyl product that was sold in the United States. This Spezyme Ethyl sample has been analyzed by me or by others working under my supervision and control. Specifically, DNA in the Spezyme Ethyl sample has been isolated, and its nucleotide sequence determined. From that analysis, I found that Spezyme Ethyl contains DNA having the nucleotide sequence set forth in Exhibit 3.

7. I or those working under my supervision and control have, moreover, analyzed the nucleotide sequence of that DNA, and have found that it encodes a protein having the amino acid sequence that is also depicted in Exhibit 3. The details of my analysis, and of the results obtained, are set forth in this Declaration.

II. DNA ANALYSIS

A. Purification of DNA from Spezyme Ethyl

8. The stability of DNA in the Spezyme Ethyl sample was tested before amplification by PCR. 10 µl of the Spezyme Ethyl sample was mixed with 10 µl of a lambda DNA size marker, BstEII digest (500 µg/ml). The mixture was incubated for one hour at room temperature, whereafter 1 µl was used for agarose gel electrophoresis. No degradation of the added lambda DNA was seen. This indicated that DNA in the Spezyme Ethyl sample is stable.

9. DNA was purified from a 100 µl aliquot of the Spezyme Ethyl sample using a QIAquick™ PCR purification kit from Quiagen, and following the manufacturer's standard protocol. Purified DNA was eluted from the kit's QIAquick columns in 50 µl of water.

B. PCR Amplification and Sequencing of Spezyme Ethyl DNA

10. The DNA molecules thus obtained were then amplified in polymerase chain reactions ("PCRs"). For these reactions, oligonucleotide primers were designed using the sequence of the gene that encodes an alpha-amylase from a natural isolate of the bacteria species *Bacillus stearothermophilus*. The cloning of this gene and its DNA sequence had previously published in a peer-reviewed scientific journal. A copy of that publication (Jorgensen *et al.*, "Cloning of a chromosomal α-amylase gene from *Bacillus stearothermophilus*", *FEMS Microbiol. Lett.* (1991) 77:271-276) is provided at Exhibit 2. Figure 2 on page 273 of the publication shows the DNA sequence of the gene (which the publication calls the "*amyS*" gene) that encodes the alpha-amylase protein from that *Bacillus stearothermophilus* isolate.

11. The oligonucleotide primers listed in Table IA, *infra*, were synthesized and used to PCR amplify the DNA purified from the Spezyme Ethyl sample. The nucleotide sequence of each primer is also set forth in Table IA, along with an indication of whether the primer was used as a forward ("F") or reverse ("R") primer for PCR. The right-hand column in Table IA specifies the nucleotides in the *amyS* gene (as set forth in Figure 2 of Exh. 2) to which each primer corresponds. Forward primers ("F") have a nucleotide sequence that is identical to the indicated portion of the *amyS* gene, whereas reverse primers ("R") have a nucleotide sequence that is identical to the indicated portion of the complementary strand.

TABLE IA:
PCR Primers to Amplify DNA
Purified from Spezyme Ethyl

Primer ID No.	Sequence	Direction (F/R)	Position
240320	5'-GATGGCACGTTATGGACC-3'	F	312-329
240321	5'-GGCGTACACTTGCATTCC-3'	R	557-540
315742	5'-CAAATCCAAGCATGGAC-3'	F	660-676
416834	5'-GTAATTGTGCAACTTGTTGATG-3'	R	1086-1064
315744	5'-GTTCGGTTTCGGTTTGG-3'	F	1681-1697
240322	5'CGAATTCACCAGTCCACG-3'	R	1767-1750

12. Additional primers, which are listed in Table IB below, were also synthesized and used to amplify DNA from the Spezyme Ethyl sample. These primers were designed to target sequences that may be upstream or downstream from alpha-amylase coding sequences in the sample. Specifically, primer nos 3626 and 3624 in Table IB correspond to known promoter sequences in the 5'-region of the *Bacillus lichenformis* alpha-amylase gene. Primer no. 414900, which is directed against other known chromosomal sequences in *Bacillus lichenformis*, was used to target sequences that may be downstream from alpha-amylase encoding sequences in the sample.

TABLE IB:
PCR Primers to Amplify DNA Purified from Spezyme Ethyl

Primer ID No.	Sequence	Direction (F/R)
3626	5'-GTCAGTCTAGAGCATGCTGGAAGAAAATATAGGG-3'	F
3624	5'-GTCAGTCTAGAGCATGCGGTACTTGTTAAAAATTC-3'	F
414900	5'-TGGTAGGCATTGCGAATGCG-3'	R

13. PCR amplifications were performed using Ready-To-Go™ PCR Beads from Amersham Pharmacia Biotech, Inc. according to the manufacturer's standard protocol. The reactions were carried out in a PTC-200® PCR machine from MJ Research with the thermocycle program set forth in Table II below:

TABLE II:
PCR Amplification Cycles Used to Amplify DNA from SPEZYEM® ETHYL

No. cycles	Temperature	Time
1 x	95 °C	2 minutes
30 x	94 °C	0.5 minutes
	(annealing)*	1 minute
	72 °C	2 minutes
1 x	72 °C	5 minutes

(*) The annealing step was carried out a different temperatures, as explained below.

14. A first PCR amplification was performed using primer nos. 3626 and 414900 from Table IB, *supra*. The PCR amplification cycle set forth in Table II was used to amplify a 10 µl aliquot of DNA purified from the Spezyme Ethyl sample. The annealing temperature was ramped down from 46 to 37 °C in increments of 1 °C, and then kept at 41 °C for the remaining

20 thermocycles. The product of this PCR reaction was then used as template for additional PCR amplifications as described below.

15. 5 µl of the PCR amplification product obtained using primer nos. 3626 and 414900 was used as template in a new PCR amplification with primer nos. 3624 and 240321 from Tables IB and IA, repsectively. The PCR amplification cycle set forth in Table II was used. The annealing temperature was ramped down from 46 to 37 °C in increments of 1 °C, and then kept at 41 °C for the remaining 20 thermocycles. Analysis of the resulting PCR product by gel electrophoresis revealed that a DNA fragment of approximately 500 bp in length had been obtained. This fragment was purified by gel electrophoresis, and its nucleotide sequence determined using the same oligonucleotides (*i.e.*, nos. 3624 and 240321) as sequencing primers in standard DNA sequencing reactions.

16. 5 µl of the PCR amplification product obtained using primer nos. 3626 and 414900 was used as template in another PCR amplification with primer nos. 240320 and 240322 from Table IA above. The PCR amplification cycle set forth in Table II was used. The annealing temperature was ramped down from 60 to 51 °C in increments of 1 °C, and then kept at 55 °C for the remaining 20 thermocycles. Analysis of the resulting PCR product by gel electrophoresis revealed that a DNA fragment about 1,500 bp in length had been obtained. This fragment was purified by gel electrophoresis, and its nucleotide sequence determined using the primer nos. 240320, 240322 and 315742 from Table IA, above, as sequencing primers in standard DNA sequencing reactions.

17. 5 µl of the PCR amplification product obtained using primer nos. 3626 and 414900 was used as template in yet another PCR amplification with primer nos. 315744 and 414900 from Tables IA and IB, respectively. The PCR amplification cycle set forth in Table II

was used. The annealing temperature was ramped down from 46 to 37 °C in increments of 1 °C, and then kept at 41 °C for the remaining 20 thermocycles. Analysis of the resulting PCR product by gel electrophoresis revealed that a DNA fragment about 200 bp in length had been obtained. This fragment was purified by gel electrophoresis, and its nucleotide sequence determined using the primer no. 315744 as the sequencing primer in a standard DNA sequencing reaction.

18. In a final PCR amplification, an another aliquot of DNA purified from the Spezyme Ethyl sample was amplified using primer nos. 240320 and 416834 from Table IA, above. The PCR amplification cycle set forth in Table II was used. The annealing temperature was ramped down from 56 to 47°C in increments of 1 °C, and then kept at 51 °C for the remaining 20 thermocycles. 5 µl of the resulting product was then used as template in an identical PCR reaction. Analysis of the resulting PCR product by gel electrophoresis revealed that a DNA fragment about 800 bp in length had been obtained. This fragment was purified by gel electrophoresis, and its nucleotide sequence determined using the primer no. 240320 as the sequencing primer in a standard DNA sequencing reaction.

19. The contiguous nucleotide sequence of the DNA in the Spezyme Ethyl sample was determined by assembling the overlapping sequences of fragments obtained from the above-described PCR reactions. The resulting DNA sequence is illustrated in the figure at Exhibit 3. Specifically, Exh. 3 shows the entire protein coding sequence of the DNA isolated from Spezyme Ethyl, aligned with its complementary sequence in the double helix.

20. The amino acid sequence encoded by this DNA was then ascertained. This amino acid sequence is also shown in Exh. 3, where it is written above the DNA sequence using the single-letter amino acid code.